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Nucleotide

□1: BC033025. Reports Homo sapiens HTPA...[gi:21542540]

```
LOCUS        BC033025               2204 bp    mRNA    linear   PRI 06-OCT-2003
DEFINITION   Homo sapiens HTPAP protein, mRNA (cDNA clone MGC:32924
             IMAGE:5267610), complete cds.
ACCESSION    BC033025
VERSION      BC033025.1  GI:21542540
KEYWORDS     MGC.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 2204)
AUTHORS      Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
             Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
             Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
             Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
             Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
             Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
             Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
             Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
             Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
             McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
             Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
             Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
             Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
             Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
             Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
             Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
             Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
```

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            TITLE        Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
                         Generation and initial analysis of more than 15,000 full-length
                         human and mouse cDNA sequences
            JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
            MEDLINE      22388257
            PUBMED       12477932
            REFERENCE    2  (bases 1 to 2204)
            AUTHORS      Strausberg,R.
            TITLE        Direct Submission
            JOURNAL      Submitted (21-JUN-2002) National Institutes of Health, Mammalian
                         Gene Collection (MGC), Cancer Genomics Office, National Cancer
                         Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                         USA
            REMARK       NIH-MGC Project URL: http://mgc.nci.nih.gov
            COMMENT      Contact: MGC help desk
                         Email: cgapbs-r@mail.nih.gov
                         Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                         cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
                         Toshiyuki and Piero Carninci (RIKEN)
                         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                         DNA Sequencing by: Institute for Systems Biology
                         http://www.systemsbiology.org
                         contact: amadan@systemsbiology.org
                         Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
                         Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

                         Clone distribution: MGC clone distribution information can be found
                         through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                         Series: IRAK Plate: 47 Row: 1 Column: 8
                         This clone was selected for full length sequencing because it
                         passed the following selection criteria: matched mRNA gi: 14210481.
                         Differences found between this sequence and the human genome (build
                         35) are described in misc_difference features below and these
                         differences were also compared to chimpanzee genomic sequences
                         available as of Sep 03, 03.
            FEATURES             Location/Qualifiers
                 source          1..2204
                                 /organism="Homo sapiens"
                                 /mol_type="mRNA"
                                 /db_xref="taxon:9606"
                                 /clone="MGC:3924 IMAGE:5267610"
                                 /tissue_type="Testis"
```

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                        /note="Vector: pBluescript"
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                        genome."
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                        /note="'G' in cDNA is 'C' in the human genome.  The
                        chimpanzee genome agrees with the cDNA sequence,
                        suggesting that this difference is unlikely to be due to
                        an artifact."
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                        /note="PAP2; Region: PAP2 superfamily. This family
                        includes the enzyme type 2 phosphatidic acid phosphatase
                        (PAP2), Glucose-6-phosphatase EC:3.1.3.9,
                        Phosphatidylglycerophosphatase B EC:3.1.3.27 and bacterial
                        acid phosphatase EC:3.1.3.2"
                        /db_xref="CDD:pfam01569"
```

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misc difference   1169..1170
                  /gene="HTPAP"
                  /note="2 bases in cDNA are not found in the human genome.
                  The chimpanzee genome agrees with the cDNA sequence,
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                  /gene="HTPAP"
                  /note="polyA tail: 17 bases do not align to the human
                  genome."

ORIGIN
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       61 ccaggcaggc gggcggcacg gggcgcgggg tcggcagtg tcggcagtg cggagctgct ccccccgttc
      121 ggcgacctgc tctgcgcttc tttgttcccc tctagggtga ctctaccgga accctacgt ggaggcggag
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      241 tatttcccca ccaagccgat gtttgttatt gcatttctct ctccactgtc tctgatcttc
      301 ctggccaaat ttctcaagaa ggcagacaca agagacagca gacaagcctg cctggctgcc
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      421 ccacgcccag atttcttcta ccgctgcttc cctgatgggc tagccattc tgacttgatg
      481 tgtacagggg ataaggacgt ggtgaatgag ggccgaaaga gcttcccag tggacattct
      541 tcctttgcat ttgctgtct ggccttttgcg tccttctacc tggcaggaa gttacactgc
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      661 tttgcagctg tgattgcact gtcccgcaca tgtgactaca agcatcactg gcaagatgta
      721 ctagttggat ccatgattgg aatgacattt gcctatgtct gctatcggca gtattatcct
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      841 cagaagcctg gggattctta ttgttttgat atttaaaaat tgaatctggc cggcgttggt
      901 ggctcatgcc tgtaatccca acactttggg aggctgagga gggtggatca cctgaggtca
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     1681 aatctagggt aattatcac tttgtgtgc atcttatctg agtccagcca tctggtactg
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```
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2101 ttatacttta aatatgacat tgtcttttat gtgtatgttc ctatatttttc aatgtatctt
2161 tttccttcag taaacctgat attcaaacaa aaaaaaaaaa aaaa
```

//

Dec 8 2004 11:02:33

Sequence Revision History

Find *(Accessions, GI numbers or Fasta style Seqlds)* BC033025

About Entrez

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	Gi	Version	Update Date
Entrez	21542540	1	Oct 6 2003 7:25 PM
	21542540	1	Jun 24 2002 4:50 PM

Search for Genes
LocusLink provides curated information for human, fruit fly, mouse, rat, and zebrafish

```
Accession = BC033025, Locus = BC033025
===========================================

Differences in LOCUS names:
-------------------------------
old: "LOCUS       BC033025          2204 bp    mRNA      linear   PRI
           24-JUN-2002"
                ^
new: "LOCUS       BC033025          2204 bp    mRNA      linear   PRI
           06-OCT-2003"
                ^

Differences in DEFINITION:
-------------------------------
old: "Homo sapiens, Similar to HTPAP protein, clone MGC:32924 IMAGE:5267610,
     mRNA, complete cds."
                                 ^
new: "Homo sapiens HTPAP protein, mRNA (cDNA clone MGC:32924 IMAGE:5267610),
     complete cds."
                 ^

Differences in REFERENCE:
-------------------------------
Changed reference:
     refline:
         old: "1  (bases 1 to 2204)"
                  ^
         new: "2  (bases 1 to 2204)"
                  ^

New reference:
```

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Batch Entrez: Upload a file of GI or accession numbers to retrieve protein or nucleotide sequences

Check sequence revision history

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LinkOut

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Related resources

BLAST

Reference sequence project

˄ LocusLink

Clusters of orthologous groups

Protein reviews on the web

```
refline:   "1  (bases 1 to 2204)"
authors:   "Strausberg,R.L., Feingold,E.A., Grouse,L.H.,
           Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L.,
           Shenmen,C.M., Schuler,G.D., Altschul,S.F.,
           Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
           Hopkins,R.F., Jordan,H., Moore,T., Max,S.I.,
           Wang,J., Hsieh,F., Diatchenko,L., Marusina,K.,
           Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M.,
           Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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           Loquellano,N.A., Peters,G.J., Abramson,R.D.,
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           Richards,S., Worley,K.C., Hale,S., Garcia,A.M.,
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           Shevchenko,Y., Bouffard,G.G., Blakesley,R.W.,
           Touchman,J.W., Green,E.D., Dickson,M.C.,
           Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
           Butterfield,Y.S., Krzywinski,M.I., Skalska,U.,
           Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J.
           and Marra,M.A."
title:     "Generation and initial analysis of more than 15,000
           full-length human and mouse cDNA sequences"
journal:   "Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
           (2002)"
muid:      "22388257"
pmid:      "12477932"

Differences in FEATURE.CDS:
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Changed feature CDS   205..876
Changed /product      =
       old: "Similar to HTPAP protein"
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       new: "HTPAP protein"
                      ^

New    /db_xref       = "LocusID:84513"
New    /gene          = "HTPAP"
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Differences in FEATURE.misc_feature:
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                          Glucose-6-phosphatase EC:3.1.3.9,
                          Phosphatidylglycerophosphatase B
                          EC:3.1.3.27 and bacterial acid phosphatase
                          EC:3.1.3.2"
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